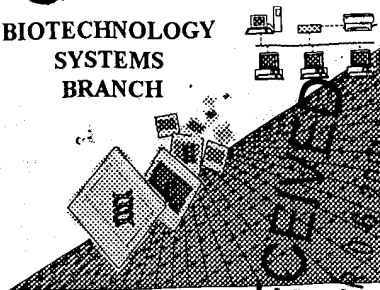


Einmann

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/673,300

Source:

1655

Date Processed by STIC:

3/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/673,300

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1655

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,300

DATE: 03/29/2001
 TIME: 10:28:05

Does Not Comply
 Corrected Diskette Needed

Input Set : A:\ES.txt
 Output Set: N:\CRF3\03292001\I673300.raw

3 <110> APPLICANT: SUNTORY LIMITED
 5 <120> TITLE OF INVENTION: Gene coding for a protein having glycosyl transferase
 6 to aurone
 8 <140> CURRENT APPLICATION NUMBER: US/09/673,300
 8 <141> CURRENT FILING DATE: 2000-10-16
 0 <130> FILE REFERENCE:
 E--> 8 <160> NUMBER OF SEQ ID NOS: 6 14 shown (see below)

see item 5
 on Error
 summary sheet

ERRORED SEQUENCES

191 <210> SEQ ID NO: 3
 192 <211> LENGTH: 25
 193 <212> TYPE: DNA
 194 <213> ORGANISM: Artificial Sequence
 196 <220> FEATURE:
 197 <223> OTHER INFORMATION: Primer
 E--> 199 <400> SEQUENCE: 36 *insert 3* 25
 200 ataactacat atgggacaac tccac
 628 <210> SEQ ID NO: 14
 629 <211> LENGTH: 23 *last sequence in file*
 630 <212> TYPE: DNA
 631 <213> ORGANISM: Artificial Sequence
 633 <220> FEATURE:
 634 <223> OTHER INFORMATION: Primer
 636 <400> SEQUENCE: 14 23
 637 ctcgtagcat ggaaaactat tct
 E--> 642 2/18
 E--> 643 1/18 *delete at end of file*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/673,300

DATE: 03/29/2001

TIME: 10:28:06

Input Set : A:\ES.txt

Output Set: N:\CRF3\03292001\I673300.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:199 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:2
L:220 M:283 W: Missing Blank Line separator, <400> field identifier
L:642 M:254 E: No. of Bases conflict, LENGTH:Input:18 Counted:24 SEQ:14
L:642 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
M:254 Repeated in SeqNo=14
L:643 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:643 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:25 SEQ:14
L:8 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (14)